

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:40:41 ; Search time 12.0465 Seconds
(Without alignments)
837.928 Million cell updates/sec

Title: US-09-622-613B-8

Perfect score: 582
Sequence: 1 MDWLTFFQKKHLNTRDVC.....TFCVTCENQAPVHFVGSHC 105

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	535	91.9	104	2 A39035	ribonuclease-relat
2	274	47.1	111	2 A27121	ribonuclease-relat
3	270.5	46.5	111	1 JX0120	ribonuclease-relat
4	254.5	43.7	111	2 JX0085	pancreatic ribonuc
5	139	23.9	119	2 S41111	pancreatic ribonuc
6	120	20.6	124	1 NRUI	pancreatic ribonuc
7	117	20.1	125	1 A32474	angiotensin (valida
8	115	19.8	128	1 NRGPB	pancreatic ribonuc
9	114	19.6	128	1 NRCU	pancreatic ribonuc
10	113	19.4	124	1 NRMHK	pancreatic ribonuc
11	109.5	18.6	145	1 A35932	angiotensin precurs
12	108	18.6	128	1 NRKS	pancreatic ribonuc
13	107	18.4	125	1 B43825	angiotensin - rabbi
14	107	18.4	138	1 NRYX	pancreatic ribonuc
15	105.5	18.1	147	2 I52489	ribonuclease 4 (EC
16	105	18.0	124	1 NRCOB	pancreatic ribonuc
17	105	18.0	124	1 NRCB	pancreatic ribonuc
18	105	18.0	124	2 JC5560	pancreatic ribonuc
19	105	18.0	124	1 NRBO	pancreatic ribonuc
20	104	17.9	124	2 S08549	ribonuclease - dom
21	103	17.7	147	1 NRHUG	angiotensin precurs
22	102	17.5	124	1 NRSH	pancreatic ribonuc
23	102	17.5	124	1 NRPRH	pancreatic ribonuc
24	102	17.5	124	1 NRHP	pancreatic ribonuc
25	102	17.5	124	2 S07141	pancreatic ribonuc
26	101.5	17.4	123	1 A43825	angiotensin - pig
27	101	17.4	124	1 NRMW	pancreatic ribonuc
28	101	17.4	124	1 NRGN	pancreatic ribonuc
29	100	17.2	124	1 NRGF	pancreatic ribonuc

30	100	17.2	124	1 NRPQ	pancreatic ribonuc
31	100	17.2	128	1 NRPO	pancreatic ribonuc
32	100	17.2	167	2 S20066	pancreatic-type ri
33	99	17.0	124	1 NRCM	pancreatic ribonuc
34	99	17.0	128	1 NRHO	pancreatic ribonuc
35	98.5	16.9	155	2 JC6159	eosinophil-associa
36	97	16.7	124	1 NRGPA	pancreatic ribonuc
37	96	16.5	124	1 NRDEO	pancreatic ribonuc
38	96	16.5	124	1 NRCMM	pancreatic ribonuc
39	96	16.5	124	1 NRCMB	pancreatic ribonuc
40	95.5	16.4	124	2 S08546	pancreatic ribonuc
41	95	16.3	124	1 NRGF	pancreatic ribonuc
42	95	16.3	156	2 JC6160	pancreatic ribonuc
43	94	16.2	124	1 NRANE	eosinophil-associa
44	93.5	16.1	119	2 JX0115	pancreatic ribonuc
45	93	16.0	124	1 NRANT	pancreatic ribonuc

ALIGNMENTS

RESULT 1

A39035 ribonuclease-related anti-tumor protein - northern leopard frog (fragment)

C:Species: Rana pipiens (northern leopard frog)

C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993

C:Accession: A39035

R:Ardelet, W., Mikulski, S.M., Shogen, K.

J. Biol. Chem. 266, 245-251, 1991

A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and e

A:Reference number: A39035; MUID:91093131; PMID:1985896

A:Accession: A39035

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-104 <ARD>

C:Superfamily: pancreatic ribonuclease

Query Match 91.9%: Score 535; DB 2; Length 104;

Best Local Similarity 92.3%: Pred. No. 2.8e-47; Mismatches 4; Indels 0; Gaps 0;

Matches 96; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY	2 QDWLTFFQKKHLNTRDVCNNILSTNLFHCKDKMTFTYSRPEPKAICGIIASKNVLT 61
DB	1 EDWLTFFQKKHLNTRDVCNNIMSTNLFHCKDKMTFTYSRPEPKAICGIIASKNVLT 60
QY	62 FEFTLSDCNVTSRCKKTKLKSTTTCVTCENQAPVHFVGSHC 105
DB	61 SEFTLSDCNVTSRCKKTKLKSTTTCVTCENQAPVHFVGSHC 104

RESULT 2

A27121 ribonuclease-related sialic acid-binding lectin - bullfrog

C:Species: Rana catesbeiana (bullfrog)

C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993

C:Accession: A27121

R:Titani, K., Takio, K., Kuwada, M., Nitta, K., Sakakibara, F., Kawuchi, H., Takayan

Biochemistry 26, 2189-2194, 1987

A:Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana

A:Reference number: A27121; MUID:87299649; PMID:3304421

A:Accession: A27121

A:Molecule type: protein

A:Residues: 1-111 <RTT>

C:Superfamily: pancreatic ribonuclease

C:Keywords: lectin

Query Match 47.1%: Score 274; DB 2; Length 111;
Best Local Similarity 46.8%: Pred. No. 8.8e-21;
Matches 52; Conservative 17; Mismatches 34; Indels 8; Gaps 3;

QY	2 QDWLTFFQKKHLNTRDVCNNILSTNLF---HCKDKMTFTYSRPEPKAICGIIASKN 57
DB	1 ENWATFOKKHLNTRDVCNNIMSTNLFYVGCKRVNTFTTSATVKAICTGVI-NMN 59

A:Accession: A32474
A:Molecule type: protein
A:Residues: 1-125 <BON>
A:Experimental source: Plasma
R:Mes: P.; Damat, D.; Rommens, C.; Montreuil, J.; Spik, G.; Tartar, A.
FEBS Lett. 241, 41-45, 1988
A:Title: The complete amino acid sequence of bovine milk angiotensin.
A:Reference number: S02001; MUID:99065101; PMID:3197838
A:Accession: S02001
A:Molecule type: protein
A:Residues: 1-125 <MAE>
A:Experimental source: milk
R:Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallée, B.L.
Submitted to the Brookhaven Protein Data Bank, January 1995
A:Reference number: A65065; PDB:1AGI
A:Contents: annotation; X-ray crystallography, 1.5 angstroms, residues 1-125
R:Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallée, B.L.
Proc. Natl. Acad. Sci. U.S.A. 92, 2949-2953, 1995
A:Title: Crystal structure of bovine angiotensin at 1.5 Angstroms resolution.
A:Reference number: A58315; MUID:95224057; PMID:7708754
A:Contents: annotation; X-ray crystallography, 1.5 angstroms
R:Leguin, O.; Albare, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
Submitted to the Brookhaven Protein Data Bank, April 1996
A:Reference number: A65709; PDB:1G10
A:Contents: annotation; conformation by (1)H-NMR, residues 1-125
R:Leguin, O.; Albare, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
Biochemistry 35, 8870-8880, 1996
A:Title: Solution structure of bovine angiotensin by (1)H nuclear magnetic resonance spect
A:Reference number: A58821; MUID:96280645; PMID:8688423
A:Contents: annotation; conformation by (1)H-NMR
R:Reisdorf, C.; Abetzel, D.; Bontems, F.; Lallemand, J.Y.; Decottignies, J.P.; Spik, G.
Eur. J. Biochem. 224, 811-822, 1994
A:Title: Proton resonance assignments and secondary structure of bovine angiotensin.
A:Reference number: S48212; MUID:95010071; PMID:7925406
A:Contents: annotation; conformation by (1)H-NMR
A:Function: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C:Superfamily: pancreatic ribonuclease
C:Keywords: angiotensin; hydrolysis; nucleic acid degradation
F:60-68/Region: receptor binding #status predicted
F:14,41,115/Active site: His, Lys, His #status predicted
F:27-82,40-93,58-108/Disulfide bonds: #status experimental

Query Match 20.1%; Score 117; DB 1; Length 125;
Best Local Similarity 32.7%; Pred. No. 8.3e-05;
Matches 32; Conservative 14; Mismatches 32; Indels 20; Gaps 5;

OY 17 DVDNNILSTNLF--HCKDKNTFYSRPEPKAIC-----GIITASKNVLTTFEY 65
DB 24 DEYCFNMKMRRLTRPCKDRNTFHKMKNDIKAIICEDRNQPYRGDLRIKSKS-----EFQ 78

OY 66 LSDC---NWSR--PCKKIKKSTITFCVTCENQAPVHF 99
DB 79 ITTCKHKGSSRPPCRGATEDSRVIVGCEGLPVHF 116

RESULT 8
NRGPB
pancreatic ribonuclease (EC 3.1.27.5) B - guinea pig (tentative sequence)
N:Alternate names: RNase IB
C:Species: *Cavia porcellus* (guinea pig)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C:Accession: A00826
R:van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gaasstra, W.; Beintema, J.J.
Eur. J. Biochem. 75, 91-100, 1977
A:Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure
A:Accession number: A91347; MUID:77185023; PMID:862624
A:Accession: A00826
A:Molecule type: protein
A:Residues: 1-128 <VAN>
A>Note: 64-Pro was also found
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas

F:12,41,119/Active site: His, Lys, His #status predicted
F:21,34/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

Query Match 19.8%; Score 115; DB 1; Length 128;
Best Local Similarity 25.9%; Pred. No. 0.00013;
Matches 30; Conservative 25; Mismatches 39; Indels 22; Gaps 7;

OY 5 LTFQKHL-----TNRDVCNNIL--STNLFHCKDKNTFYSRPEPKAIC--KGI 53
DB 6 MKFQKHMDPEGSESSNNT--CNVMMIRNMTGCRCKPVNTFVHESLADYQVCFQKNVL 64

OY 54 ASKNVLTTFEY-----LSDCNWTSR---CKYLLKSTITFCVTCENQ--APVHF 99
DB 65 CKNGQTCYQSYSMRTITDCRVSSSKFPMCSYMSQAQSIIVACGDPYVPHF 120

RESULT 9
NRCU
pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)
N:Alternate names: RNase 1; RNase A
C:Species: *Mycastor coypus* (nutria, coypu)
C:Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C:Accession: A00822
R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A:Title: Isolation, properties and primary structure of coypu and chinchilla pancreat
A:Reference number: A90612; MUID:77065676; PMID:999896
A:Accession: A00822
A:Molecule type: protein
A:Residues: 1-128 <VAN>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,41,119/Active site: His, Lys, His #status predicted
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 19.6%; Score 114; DB 1; Length 128;
Best Local Similarity 28.2%; Pred. No. 0.00017;
Matches 33; Conservative 19; Mismatches 37; Indels 28; Gaps 7;

OY 7 FQKHL-----TNRDVCNNIL--STNLF--HCKDKNTFYSRPEPKAICGIITASKNV 58
DB 8 FERQHMDSRGSPTRPNYCNEMKSRMNTGCRCKPVNTFVHEPLADYQAVC----FQKNV 63

OY 59 L-----TTFEPLSDCNVTSR---CKKIKKSTITFCVTCENQ--AAVHF 99
DB 64 LCKNGQTCYQSYSMNMTITDCRVTSNSDPNCSYRTSOEKSIVVACGDPYVPHF 120

RESULT 10
NRMHK
pancreatic ribonuclease (EC 3.1.27.5) - mink whale
N:Alternate names: RNase A
C:Species: *Balaenoptera acutorostrata* (mink whale, lesser rorqual)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C:Accession: A00818
R:Emmens, M.; Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
A:Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclea
A:Reference number: A00818; MUID:76277855; PMID:962870
A:Accession: A00818
A:Molecule type: protein
A:Residues: 1-124 <EMK>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,41,119/Active site: His, Lys, His #status predicted
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F:76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 19.4%; Score 113; DB 1; Length 124;
Best Local Similarity 26.9%; Pred. No. 0.00021;
Matches 32; Conservative 16; Mismatches 43; Indels 28; Gaps 6;

Db 66 KNGQINCYOSYSMSHITDCRVTNSKFPDCSYRTTOAKRSIVVACEGNLYVPVHF 120

RESULT 15

152489

ribonuclease 4 (EC 3.1.-.-) precursor - human

N:Alternate names: RNase 4

C:Species: Homo sapiens (man)

C:Date: 02-Jul-1996 #sequence.revision 02-Jul-1996 #text_change 22-Jun-1999

C:Accession: I52489; S60163; S38272

R:seno, M.; Futami, J.; Tsushima, Y.; Akutagawa, K.; Kosaka, M.; Tada, H.; Yamada, H.

Biochim. Biophys. Acta 1261, 424-426, 1995

A:title: Molecular cloning and expression of human ribonuclease 4 cDNA.

A:Reference number: I52489; MUID:95260866; PMID:7742370

A:Accession: I52489

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-147 <RES>

A:Cross-references: GB:D37931; NID:9976228; PIDN:BAA07150.1; PID:9976229

R:Rosenberg, H.F.; Dyer, K.D.

Nucleic Acids Res. 23, 4290-4295, 1995

A:title: Human ribonuclease 4 (RNase 4): coding sequence, chromosomal localization and

A:Reference number: S60163; MUID:96091174; PMID:7501448

A:Accession: S60163

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 29-53, 'D', '55-147' <ROS>

A:Cross-references: EMBL:U36775; NID:91040977; PIDN:AAA96750.1; PID:91040978

R:Zhou, H.M.; Stridom, D.U.

Eur. J. Biochem. 217, 401-410, 1993

A:title: The amino acid sequence of human ribonuclease 4, a highly conserved ribonuclease

A:Reference number: S38272; MUID:94039064; PMID:8223579

A:Accession: S38272

A:Molecule type: protein

A:Residues: 29-147 <ZHO>

C:Genetics:

A:Gene: GDB:RNASE4

A:Cross-references: GDB:6108046; OMIM:601030

A:Map position: 14q24-q31

A:Introns: #status absent

C:Superfamily: pancreatic ribonuclease

C:Keywords: hydrolase

F:40,68,144/Active site: His, Lys, His #status predicted

F:53-109,67-120,85-135,92-99/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 31.2%; Score 105.5; DB 2; Length 147;

Matches 35; Conservative 16; Mismatches 44; Indels 17; Gaps 7;

QY 7 FOKKHL---TNTRDVDCNNITL---STNLFHCKDKNTFIYSRPEPKAIKK--GIISKN 57
 Db 36 FLROHVPRETTGSDYRCNLMORRKMTLYHCKRFTFIHEDTWNIRISICSTINIOCKNG 95
 QY 58 VLTTFE--FYLSDCNVT--SRP--CKYKIKKSTITFCVTCEN--QAPVHFVG 101
 Db 96 KMNCHGVVAVTDCRDTGSSRAPNCRVRAIASTRRVVIACEGNPOVPVHFHDG 147

Search completed: June 25, 2003, 14:58:02
 Job time : 12.0465 secs

